

1/10

Figure 1B

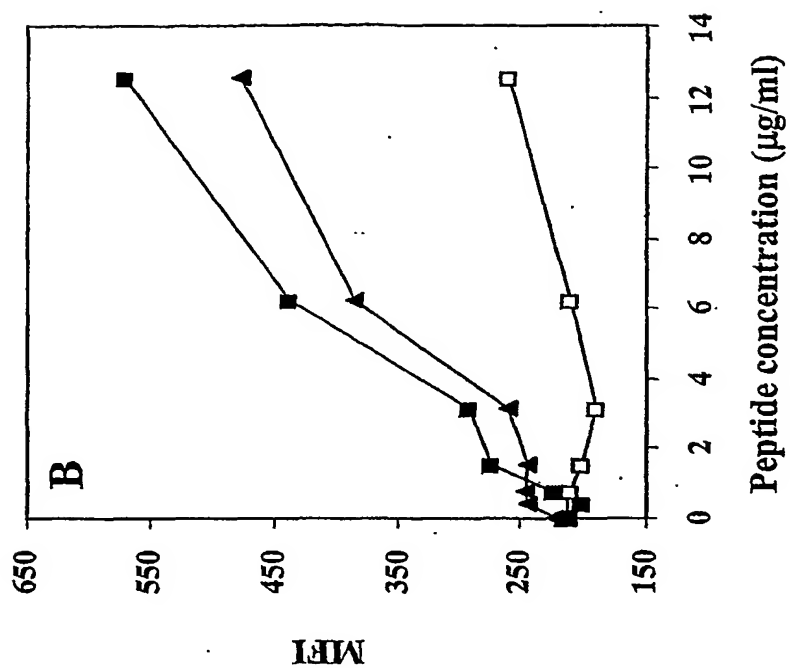
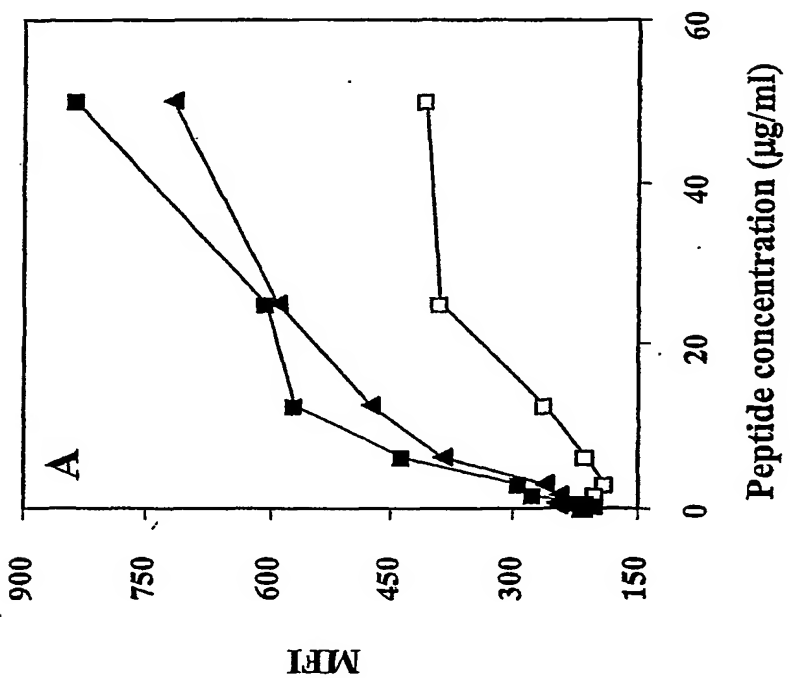
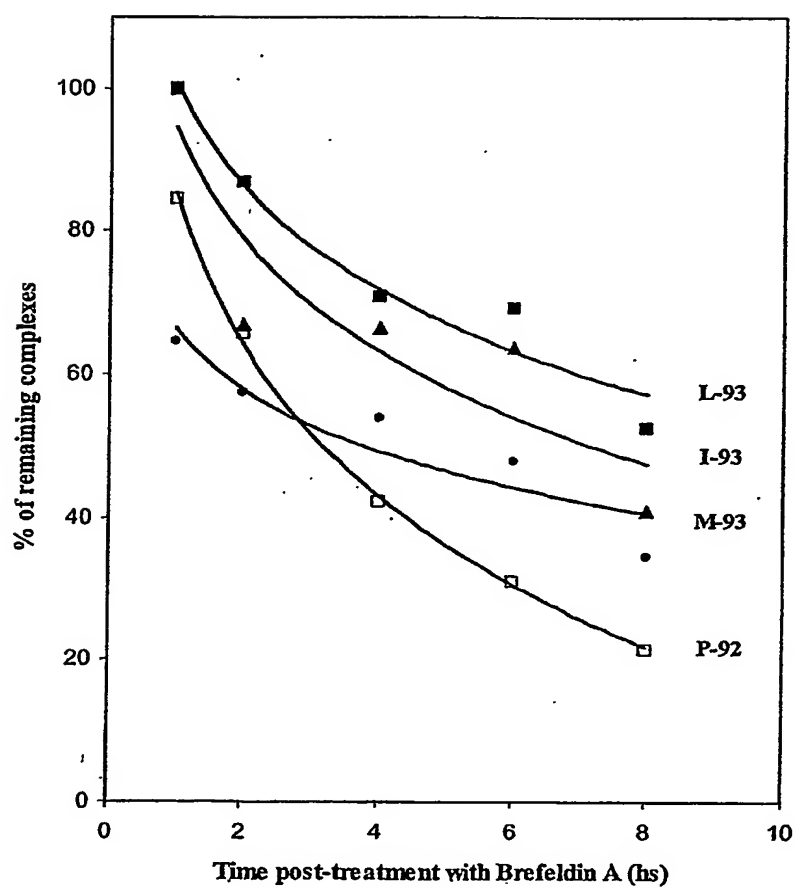


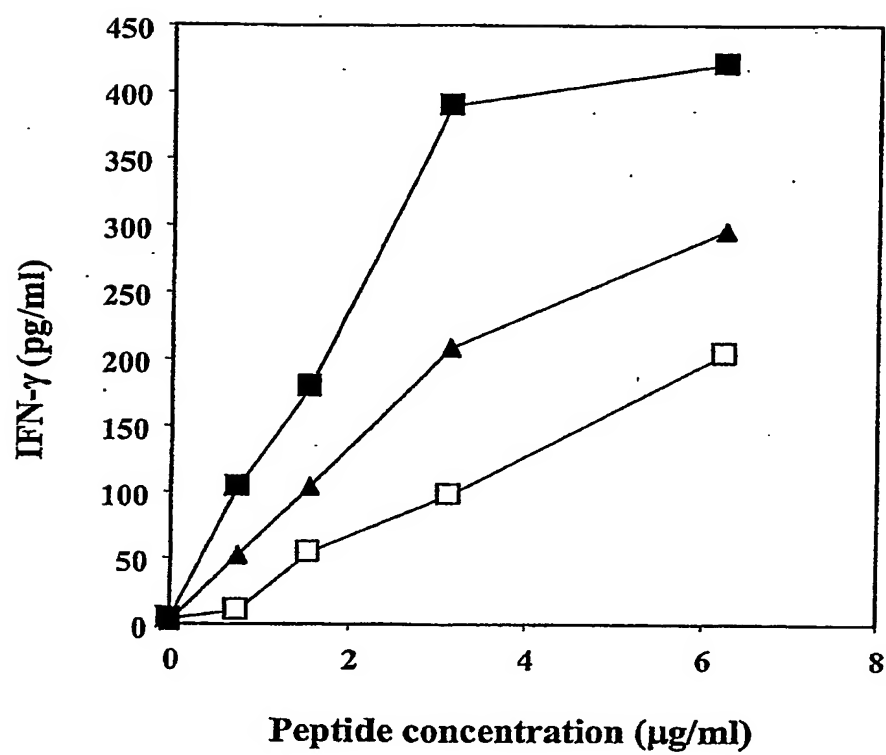
Figure 1A



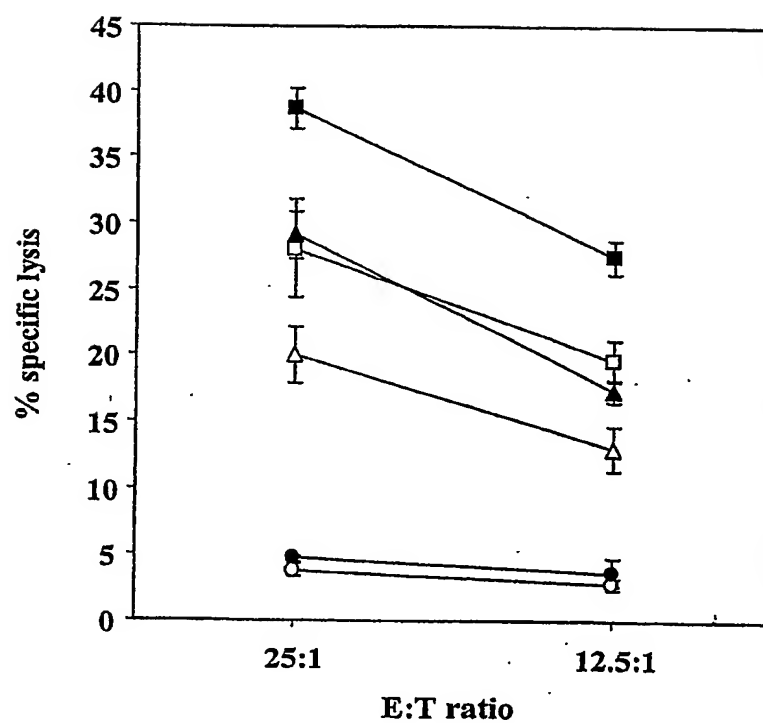
2/10

Figure 2

3/10

Figure 3

4/10

Figure 4

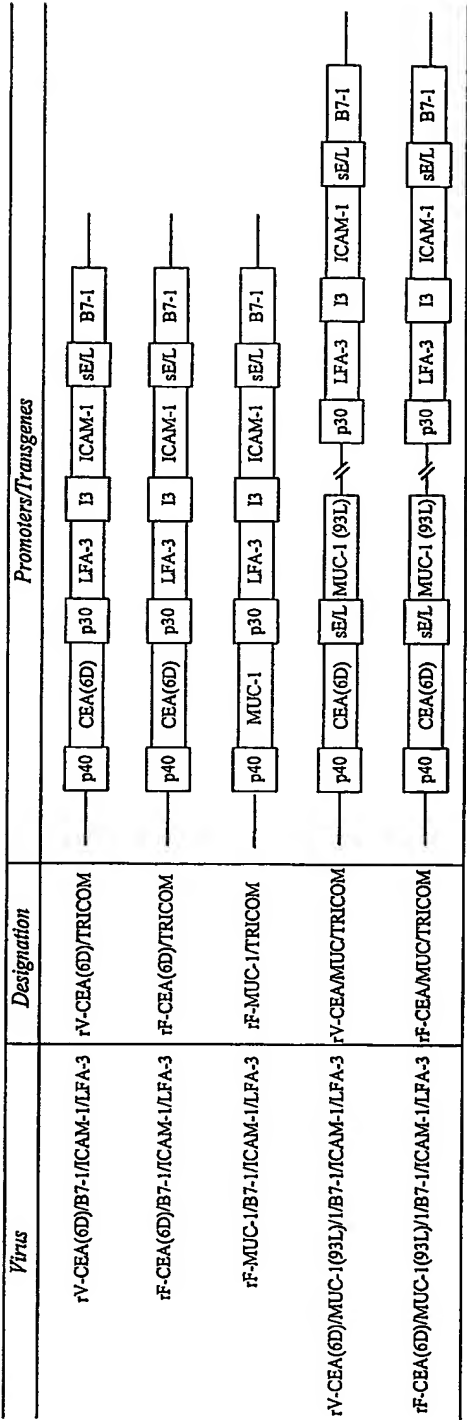
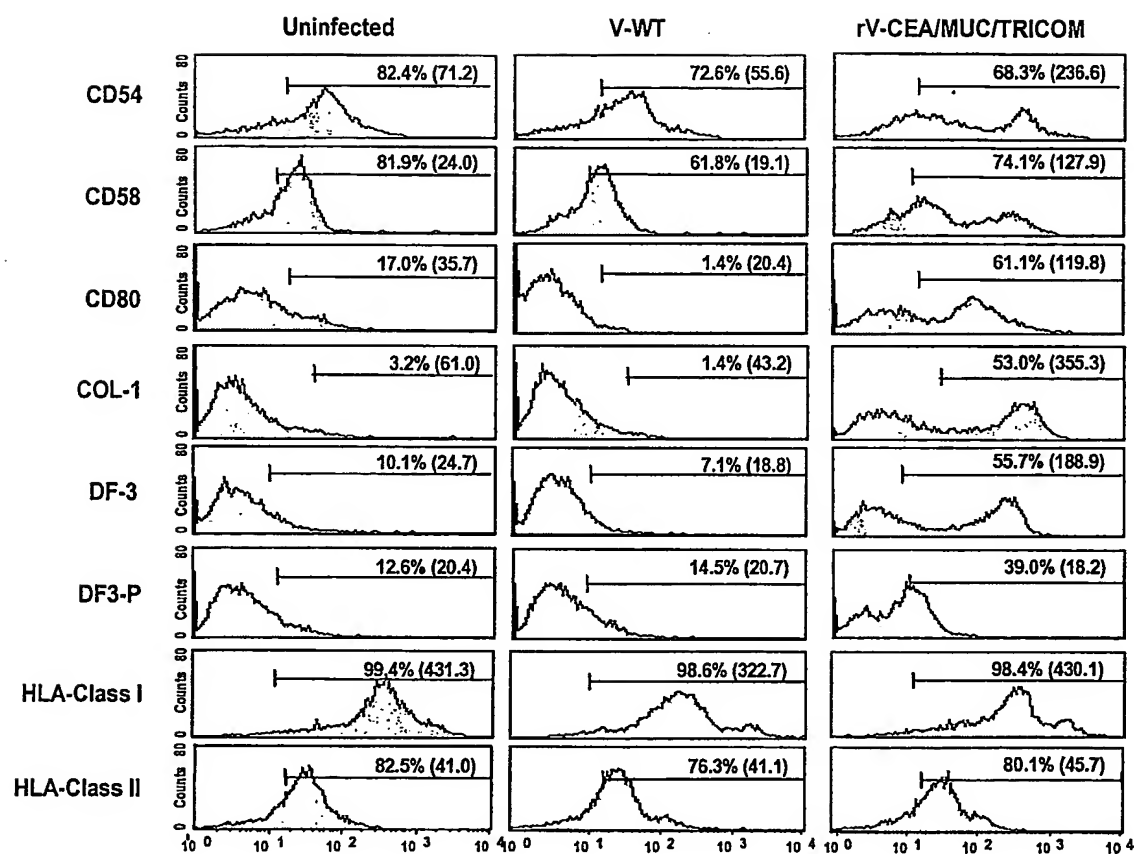
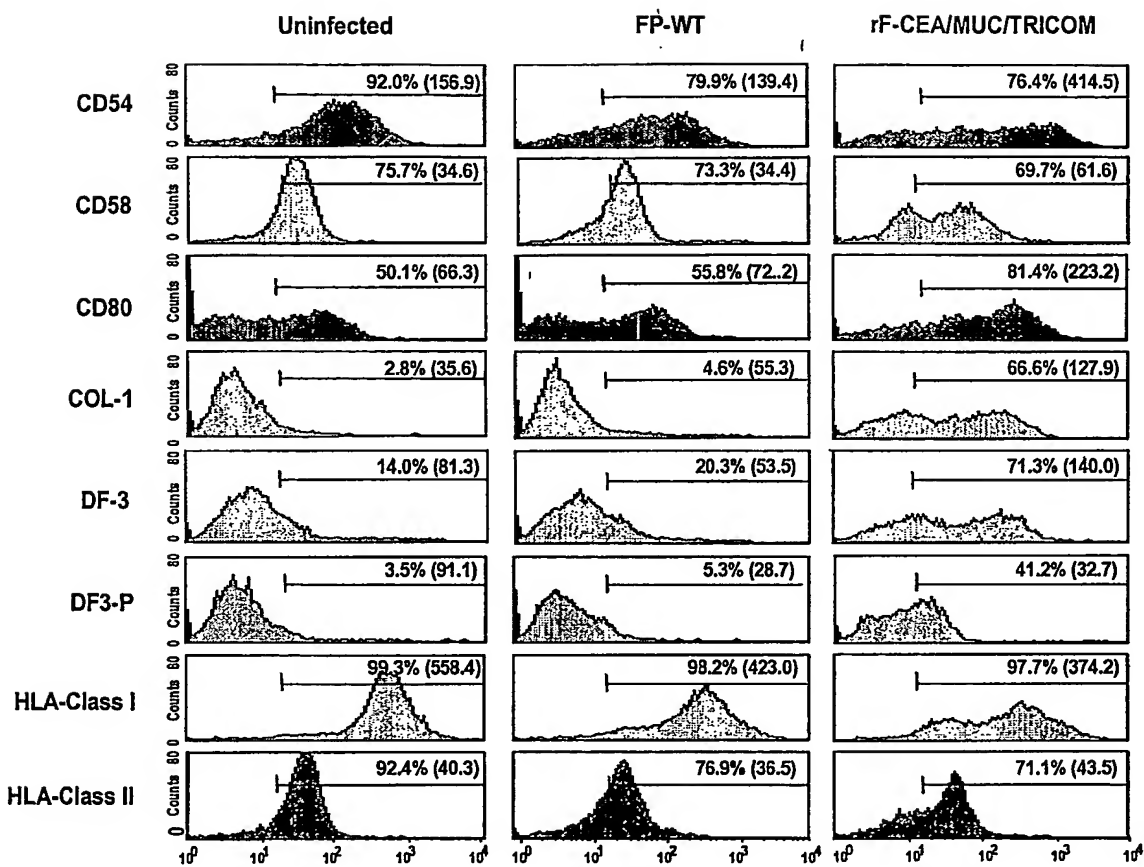


Figure 5

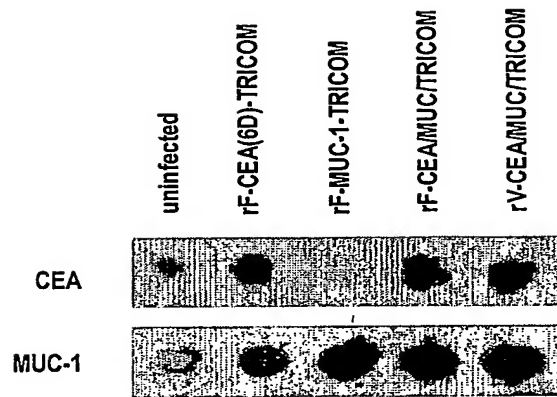
6/10

**Figure 6**

7/10

**Figure 7**

8/10

**Figure 8**

9/10

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 61 GTTACGGGTT CTGGTCATGC AAGCTCTACC CCAGGTGGAG AAAGGAGAC TTCGGCTACC
 121 CAGAGAGATT CAGTCCCCAG CTCATCTGAG AGAATCTG AGAATCTG TGGTATGAC AAGCTCCGTA
 181 CTCTCCAGCC ACAGCCCGG TTCAGGCTCC TCACACCACTC AGGACACGA TGTCACTCTG
 241 GCCCCGCCA CCGAACCCAG CTCAGGTTCA GCTGCCCTGT GGGACACGA TGTCACTCTG
 301 GTACCACTTA CTAGACCCAG TTAGGTAGC ACAGCACCTC CCGCACATGG CGTACATCA
 361 GCTCTGATA CTCGTCCAGC TCTGGCAGT ACTGCACAC CTGBCACCG AGTGACATCG
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 781 ACTCTACCA CCGTGCAG CCAAGCACT CCACTTCORA TTCCACGCCA CCACTCTGAT
 841 ACGGTACCTC CTCTCACCTC CTCACATCAC AGCACTGTC CCGGTCTTC TACTGGGAT
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Figure 9

10/10

Figure 10

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 GTSA PDTRPAPASTLVHNGTSARATTPASKSTPFPSHSDPTTLASHST
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